

Nuno Sepúlveda

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

3,333
citations

186265

28
h-index

189892

50
g-index

102
all docs

102
docs citations

102
times ranked

6011
citing authors

#	ARTICLE	IF	CITATIONS
1	A Central Role for Free Heme in the Pathogenesis of Severe Sepsis. <i>Science Translational Medicine</i> , 2010, 2, 51ra71.	12.4	412
2	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019, 51, 51-62.	21.4	328
3	Reappraisal of known malaria resistance loci in a large multicenter study. <i>Nature Genetics</i> , 2014, 46, 1197-1204.	21.4	206
4	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	21.4	91
5	Human candidate gene polymorphisms and risk of severe malaria in children in Kilifi, Kenya: a case-control association study. <i>Lancet Haematology</i> , 2018, 5, e333-e345.	4.6	90
6	European Network on Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (EUROMENE): Expert Consensus on the Diagnosis, Service Provision, and Care of People with ME/CFS in Europe. <i>Medicina (Lithuania)</i> , 2021, 57, 510.	2.0	89
7	<i>Plasmodium falciparum</i> parasites with histidine-rich protein 2 (pfrp2) and pfrp3 gene deletions in two endemic regions of Kenya. <i>Scientific Reports</i> , 2017, 7, 14718.	3.3	85
8	Glucose-6-phosphate dehydrogenase deficiency and the risk of malaria and other diseases in children in Kenya: a case-control and a cohort study. <i>Lancet Haematology</i> , 2015, 2, e437-e444.	4.6	74
9	The low-virulent African swine fever virus (ASFV/NH/P68) induces enhanced expression and production of relevant regulatory cytokines (IFN γ , TNF α and IL12p40) on porcine macrophages in comparison to the highly virulent ASFV/L60. <i>Archives of Virology</i> , 2008, 153, 1845-1854.	2.1	64
10	Characterisation of the opposing effects of G6PD deficiency on cerebral malaria and severe malarial anaemia. <i>ELife</i> , 2017, 6, .	6.0	64
11	When three is not a crowd: a Crossregulation Model of the dynamics and repertoire selection of regulatory CD4 ⁺ T cells. <i>Immunological Reviews</i> , 2007, 216, 48-68.	6.0	63
12	Variation in natural exposure to anopheles mosquitoes and its effects on malaria transmission. <i>ELife</i> , 2018, 7, .	6.0	60
13	African Glucose-6-Phosphate Dehydrogenase Alleles Associated with Protection from Severe Malaria in Heterozygous Females in Tanzania. <i>PLoS Genetics</i> , 2015, 11, e1004960.	3.5	58
14	Cellular Immune Function in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS). <i>Frontiers in Immunology</i> , 2019, 10, 796.	4.8	56
15	Novel genetic polymorphisms associated with severe malaria and under selective pressure in North-eastern Tanzania. <i>PLoS Genetics</i> , 2018, 14, e1007172.	3.5	55
16	Optimisation and standardisation of a multiplex immunoassay of diverse <i>Plasmodium falciparum</i> antigens to assess changes in malaria transmission using sero-epidemiology. <i>Wellcome Open Research</i> , 2019, 4, 26.	1.8	52
17	Serology describes a profile of declining malaria transmission in Farafenni, The Gambia. <i>Malaria Journal</i> , 2015, 14, 416.	2.3	49
18	Transforming Growth Factor Beta 2 and Heme Oxygenase 1 Genes Are Risk Factors for the Cerebral Malaria Syndrome in Angolan Children. <i>PLoS ONE</i> , 2010, 5, e11141.	2.5	47

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19	Candidate Polymorphisms and Severe Malaria in a Malian Population. PLoS ONE, 2012, 7, e43987.	2.5	41
20	A novel multiplex qPCR assay for detection of Plasmodium falciparum with histidine-rich protein 2 and 3 (pfrp2 and pfrp3) deletions in polyclonal infections. EBioMedicine, 2020, 55, 102757.	6.1	41
21	Systematic Review of the Epidemiological Burden of Myalgic Encephalomyelitis/Chronic Fatigue Syndrome Across Europe: Current Evidence and EUROMENE Research Recommendations for Epidemiology. Journal of Clinical Medicine, 2020, 9, 1557.	2.4	41
22	Global analysis of Plasmodium falciparum histidine-rich protein-2 (pfrp2) and pfrp3 gene deletions using whole-genome sequencing data and meta-analysis. Infection, Genetics and Evolution, 2018, 62, 211-219.	2.3	40
23	Optimisation and standardisation of a multiplex immunoassay of diverse Plasmodium falciparum antigens to assess changes in malaria transmission using sero-epidemiology. Wellcome Open Research, 2019, 4, 26.	1.8	40
24	Candidate Human Genetic Polymorphisms and Severe Malaria in a Tanzanian Population. PLoS ONE, 2012, 7, e47463.	2.5	39
25	Relevance of feline interferon omega for clinical improvement and reduction of concurrent viral excretion in retrovirus infected cats from a rescue shelter. Research in Veterinary Science, 2013, 94, 753-763.	1.9	38
26	Biochemical and ecophysiological responses to manganese stress by ectomycorrhizal fungus Pisolithus tinctorius and in association with Eucalyptus grandis. Mycorrhiza, 2016, 26, 475-487.	2.8	38
27	Current Mathematical Models for Analyzing Anti-Malarial Antibody Data with an Eye to Malaria Elimination and Eradication. Journal of Immunology Research, 2015, 2015, 1-21.	2.2	37
28	Expression at mRNA level of cytokines and A238L gene in porcine blood-derived macrophages infected in vitro with African swine fever virus (ASFV) isolates of different virulence. Archives of Virology, 2003, 148, 2077-2097.	2.1	35
29	Human Candidate Polymorphisms in Sympatric Ethnic Groups Differing in Malaria Susceptibility in Mali. PLoS ONE, 2013, 8, e75675.	2.5	35
30	Glucose-6-phosphate dehydrogenase polymorphisms and susceptibility to mild malaria in Dogon and Fulani, Mali. Malaria Journal, 2014, 13, 270.	2.3	34
31	Characterizing the impact of sustained sulfadoxine/pyrimethamine use upon the Plasmodium falciparum population in Malawi. Malaria Journal, 2016, 15, 575.	2.3	34
32	Differentiation of human thymic regulatory T cells at the double positive stage. European Journal of Immunology, 2011, 41, 3604-3614.	2.9	32
33	Myalgic Encephalomyelitis/Chronic Fatigue Syndrome as a Hyper-Regulated Immune System Driven by an Interplay Between Regulatory T Cells and Chronic Human Herpesvirus Infections. Frontiers in Immunology, 2019, 10, 2684.	4.8	30
34	Serologically Defined Variations in Malaria Endemicity in Pará State, Brazil. PLoS ONE, 2014, 9, e113357.	2.5	30
35	Estimation of T-cell repertoire diversity and clonal size distribution by Poisson abundance models. Journal of Immunological Methods, 2010, 353, 124-137.	1.4	28
36	Serology reflects a decline in the prevalence of trachoma in two regions of The Gambia. Scientific Reports, 2017, 7, 15040.	3.3	28

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37	Oral Recombinant Feline Interferon-Omega as an alternative immune modulation therapy in FIV positive cats: Clinical and laboratory evaluation. <i>Research in Veterinary Science</i> , 2014, 96, 79-85.	1.9	27
38	Sample size determination for estimating antibody seroconversion rate under stable malaria transmission intensity. <i>Malaria Journal</i> , 2015, 14, 141.	2.3	27
39	Fc gamma Receptor γ 131 Polymorphism and Malaria Susceptibility in Sympatric Ethnic Groups, Fulani and Dogon of Mali. <i>Scandinavian Journal of Immunology</i> , 2014, 79, 43-50.	2.7	26
40	Genetic determinants of anti-malarial acquired immunity in a large multi-centre study. <i>Malaria Journal</i> , 2015, 14, 333.	2.3	26
41	Novel Insights Into the Protective Role of Hemoglobin S and C Against <i>Plasmodium falciparum</i> Parasitemia. <i>Journal of Infectious Diseases</i> , 2015, 212, 626-634.	4.0	26
42	USP38, FREM3, SDC1, DDC, and LOC727982 Gene Polymorphisms and Differential Susceptibility to Severe Malaria in Tanzania. <i>Journal of Infectious Diseases</i> , 2015, 212, 1129-1139.	4.0	26
43	A Bayesian Semiparametric Approach for the Differential Analysis of Sequence Counts Data. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2014, 63, 385-404.	1.0	24
44	Genetic control of parasite clearance leads to resistance to <i>Plasmodium berghei</i> ANKA infection and confers immunity. <i>Genes and Immunity</i> , 2005, 6, 416-421.	4.1	23
45	Evaluation of viremia, proviral load and cytokine profile in naturally feline immunodeficiency virus infected cats treated with two different protocols of recombinant feline interferon omega. <i>Research in Veterinary Science</i> , 2015, 99, 87-95.	1.9	23
46	Effectiveness of a serological tool to predict malaria transmission intensity in an elimination setting. <i>BMC Infectious Diseases</i> , 2017, 17, 49.	2.9	23
47	Mechanisms Controlling Termination of V-J Recombination at the TCR β Locus: Implications for Allelic and Isotypic Exclusion of TCR β Chains. <i>Journal of Immunology</i> , 2005, 174, 3912-3919.	0.8	22
48	Highly Dynamic Host Actin Reorganization around Developing <i>Plasmodium</i> Inside Hepatocytes. <i>PLoS ONE</i> , 2012, 7, e29408.	2.5	22
49	Quality control of multiplex antibody detection in samples from large-scale surveys: the example of malaria in Haiti. <i>Scientific Reports</i> , 2020, 10, 1135.	3.3	22
50	Arbuscular mycorrhizal fungi induce differential activation of the plasma membrane and vacuolar H ⁺ pumps in maize roots. <i>Mycorrhiza</i> , 2009, 19, 69-80.	2.8	21
51	Monitoring acute phase proteins in retrovirus infected cats undergoing feline interferon γ therapy. <i>Journal of Small Animal Practice</i> , 2014, 55, 39-45.	1.2	20
52	The NF- κ B Canonical Pathway Is Involved in the Control of the Exonucleolytic Processing of Coding Ends during V(D)J Recombination. <i>Journal of Immunology</i> , 2008, 180, 1040-1049.	0.8	19
53	A Poisson hierarchical modelling approach to detecting copy number variation in sequence coverage data. <i>BMC Genomics</i> , 2013, 14, 128.	2.8	19
54	Prevalence and incidence of myalgic encephalomyelitis/chronic fatigue syndrome in Europe—the Euro-epiME study from the European network EUROMENE: a protocol for a systematic review. <i>BMJ Open</i> , 2018, 8, e020817.	1.9	19

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55	Ocular Chlamydia trachomatis infection, anti-Pgp3 antibodies and conjunctival scarring in Vanuatu and Tarawa, Kiribati before antibiotic treatment for trachoma. <i>Journal of Infection</i> , 2020, 80, 454-461.	3.3	19
56	Association between the proportion of Plasmodium falciparum and Plasmodium vivax infections detected by passive surveillance and the magnitude of the asymptomatic reservoir in the community: a pooled analysis of paired health facility and community data. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 953-963.	9.1	18
57	Sample size and power calculations for detecting changes in malaria transmission using antibody seroconversion rate. <i>Malaria Journal</i> , 2015, 14, 529.	2.3	17
58	Herpesviruses Serology Distinguishes Different Subgroups of Patients From the United Kingdom Myalgic Encephalomyelitis/Chronic Fatigue Syndrome Biobank. <i>Frontiers in Medicine</i> , 2021, 8, 686736.	2.6	17
59	Stochastic Modeling of T cell receptor gene rearrangement. <i>Journal of Theoretical Biology</i> , 2005, 234, 153-165.	1.7	15
60	Surveillance of Aedes aegypti populations in the city of Praia, Cape Verde: Zika virus infection, insecticide resistance and genetic diversity. <i>Parasites and Vectors</i> , 2020, 13, 481.	2.5	15
61	Assessing Incidence Patterns and Risk Factors for Cutaneous Leishmaniasis in Peshawar Region, Khyber Pakhtunkhwa, Pakistan. <i>Journal of Parasitology</i> , 2016, 102, 501-506.	0.7	14
62	Evaluation of the humoral immune response induced by vaccination for canine distemper and parvovirus: a pilot study. <i>BMC Veterinary Research</i> , 2018, 14, 348.	1.9	14
63	Delineating the Association Between Soluble CD26 and Autoantibodies Against G-Protein Coupled Receptors, Immunological and Cardiovascular Parameters Identifies Distinct Patterns in Post-Infectious vs. Non-Infection-Triggered Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. <i>Frontiers in Immunology</i> , 2021, 12, 644548.	4.8	14
64	Malaria Host Candidate Genes Validated by Association With Current, Recent, and Historical Measures of Transmission Intensity. <i>Journal of Infectious Diseases</i> , 2017, 216, 45-54.	4.0	13
65	Allelic penetrance approach as a tool to model two-locus interaction in complex binary traits. <i>Heredity</i> , 2007, 99, 173-184.	2.6	12
66	Failure of rapid diagnostic tests in Plasmodium falciparum malaria cases among travelers to the UK and Ireland: Identification and characterisation of the parasites. <i>International Journal of Infectious Diseases</i> , 2021, 108, 137-144.	3.3	12
67	Decreased NO production in endothelial cells exposed to plasma from ME/CFS patients. <i>Vascular Pharmacology</i> , 2022, 143, 106953.	2.1	11
68	Detection and modeling of anti-Leptospira IgG prevalence in cats from Lisbon area and its correlation to retroviral infections, lifestyle, clinical and hematologic changes. <i>Veterinary and Animal Science</i> , 2020, 10, 100144.	1.5	10
69	Pharmacodynamics and cellular accumulation of amphotericin B and miltefosine in Leishmania donovani-infected primary macrophages. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1314-1323.	3.0	9
70	Review of the Quality Control Checks Performed by Current Genome-Wide and Targeted-Genome Association Studies on Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. <i>Frontiers in Pediatrics</i> , 2020, 8, 293.	1.9	9
71	A potential antigenic mimicry between viral and human proteins linking Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) with autoimmunity: The case of HPV immunization. <i>Autoimmunity Reviews</i> , 2020, 19, 102487.	5.8	9
72	Lessons From Heat Stroke for Understanding Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. <i>Frontiers in Neurology</i> , 2021, 12, 789784.	2.4	8

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73	Comparison of Commercial ELISA Kits to Confirm the Absence of Transmission in Malaria Elimination Settings. <i>Frontiers in Public Health</i> , 2020, 8, 480.	2.7	7
74	The SARS-CoV-2 receptor angiotensin-converting enzyme 2 (ACE2) in myalgic encephalomyelitis/chronic fatigue syndrome: A meta-analysis of public DNA methylation and gene expression data. <i>Heliyon</i> , 2021, 7, e07665.	3.2	7
75	Revisiting IgG Antibody Reactivity to Epstein-Barr Virus in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome and Its Potential Application to Disease Diagnosis. <i>Frontiers in Medicine</i> , 0, 9, .	2.6	7
76	Heterogeneous malaria transmission in long-term Afghan refugee populations: a cross-sectional study in five refugee camps in northern Pakistan. <i>Malaria Journal</i> , 2016, 15, 245.	2.3	6
77	On the Performance of Multiple Imputation Based on Chained Equations in Tackling Missing Data of the African α -Globin Deletion in a Malaria Association Study. <i>Annals of Human Genetics</i> , 2014, 78, 277-289.	0.8	5
78	Scrapie genetic susceptibility in Portuguese sheep breeds. <i>Veterinary Record</i> , 2003, 153, 508.	0.3	5
79	Bayesian analysis of allelic penetrance models for complex binary traits. <i>Computational Statistics and Data Analysis</i> , 2009, 53, 1271-1283.	1.2	4
80	Allele-specific antibodies to Plasmodium vivax merozoite surface protein-1: prevalence and inverse relationship to haemoglobin levels during infection. <i>Malaria Journal</i> , 2016, 15, 559.	2.3	4
81	Impact of genetic variation on the molecular mimicry between Anoctamin-2 and Epstein-Barr virus nuclear antigen 1 in Multiple Sclerosis. <i>Immunology Letters</i> , 2021, 238, 29-31.	2.5	4
82	A statistical analysis of serological data from the UK myalgic encephalomyelitis/chronic fatigue syndrome biobank. <i>AIP Conference Proceedings</i> , 2020, , .	0.4	3
83	Dynamics of Peripheral Regulatory and Effector T Cells Competing for Antigen Presenting Cells. , 2011, , 275-303.		2
84	Plasmodium malariae and Plasmodium ovale infections and their association with common red blood cell polymorphisms in a highly endemic area of Uganda. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2019, 113, 370-378.	1.8	2
85	Editorial: Current Insights Into Complex Post-infection Fatigue Syndromes With Unknown Aetiology: The Case of Myalgic Encephalomyelitis/Chronic Fatigue Syndrome and Beyond. <i>Frontiers in Medicine</i> , 2022, 9, 862953.	2.6	2
86	Sero-epidemiological study of arbovirus infection following the 2015â€“2016 Zika virus outbreak in Cabo Verde. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
87	G6PD Polymorphisms and Hemolysis After Antimalarial Treatment With Low Single-Dose Primaquine: A Pooled Analysis of Six African Clinical Trials. <i>Frontiers in Genetics</i> , 2021, 12, 645688.	2.3	1
88	Assessment of malaria transmission intensity using anti-MSP1-19 (Plasmodium vivax) antibody as a serological marker in a previously malaria endemic district in Sri Lanka. <i>International Journal of Infectious Diseases</i> , 2016, 45, 362.	3.3	0
89	Bayesian Genetic Mapping of Binary Trait Loci. , 2013, , 139-146.		0